

Please amend the beginning on line 18 or page 5 to read as follows:

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Figure 1A and 1B show the 14926 nucleotide sequence (SEQ ID NO:2) and the deduced 14926 amino acid sequence (SEQ ID NO:1). It is predicted that amino acids 1-23 constitute the amino terminal extracellular domain, amino acids 24-341 constitute the region spanning the transmembrane domain, and amino acids 342-370 constitute the carboxy terminal intracellular domain. The transmembrane domain contains seven transmembrane segments, three extracellular loops and three intracellular loops. The transmembrane segments are found from about amino acid 24 to about amino acid 46, from about amino acid 56 to about amino acid 78, from about amino acid 96 to about amino acid 117, from about amino acid 133 to about amino acid 154, from about amino acid 185 to about amino acid 209, from about amino acid 286 to about amino acid 307, and from about amino acid 318 to about amino acid 341. Within the region spanning the entire transmembrane domain are three intracellular and three extracellular loops. The three intracellular loops are found from about amino acid 47 to about amino acid 55, from about amino acid 118 to about amino acid 132, and from about amino acid 210 to about amino acid 285. The three extracellular loops are found at from about amino acid 79 to about amino acid 95, from about amino acid 155 to about amino acid 184, and from about amino acid 308 to about amino acid 317.

Please amend the paragraph beginning on line 26 of page 6 as follows:

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Figure 5A and 5B show an analysis of the 14926 open reading frame for amino acids corresponding to specific functional sites. A glycosylation site is found at amino acids 3-6, which corresponds to the amino terminal extracellular domain. A second glycosylation site is found at amino acids 83-86, which corresponds to the first extracellular loop. A third glycosylation site is found at amino acids 182-185, which spans the second extracellular loop and fifth transmembrane segment. A fourth glycosylation site is found at amino acids 227-230, which corresponds to the third intracellular loop. A fifth glycosylation site occurs at amino acids 264-267, also in the third intracellular loop. A cyclic AMP or cyclic GMP-dependent protein kinase phosphorylation site is found at amino acids 131-134 and spans the second intracellular

loop and fourth transmembrane segment, and at amino acids 281-284, corresponding to the third intracellular loop. A protein kinase C phosphorylation site is found at amino acids 80-82, corresponding to the first intracellular loop. A second protein kinase C phosphorylation site is found at amino acids 93-95, corresponding to the first extracellular loop. A third protein kinase C phosphorylation site is found at amino acids 130-132, corresponding to the second intracellular loop. A fourth protein kinase C phosphorylation site is found at amino acids 178-180, corresponding to the second extracellular loop. A fifth protein kinase C phosphorylation site is found at amino acids 266-268, corresponding to the third intracellular loop. A sixth protein kinase C phosphorylation site is found at amino acids 342-344, corresponding to the carboxy terminal intracellular domain. A casein kinase II phosphorylation site occurs at amino acids 342-345, corresponding to the carboxy terminal intracellular domain. N-myristoylation sites occur at amino acids 84-89 and 90-95, corresponding to the first extracellular loop; 101-106, corresponding to the third transmembrane segment; 237-242 and 258-263, corresponding to the third intracellular loop; and 318-323, corresponding to the seventh transmembrane segment. An amidation site is found at amino acids 266-269, corresponding to the third intracellular loop. In addition, amino acids corresponding in position to the GPCR signature and containing the invariant arginine are found in the sequence TRY at amino acids 118-120.

Please amend the paragraph on lines 4-6 of page 10 to read as follows:

B₆ The invention thus relates to a novel GPCR having the deduced amino acid sequence shown in Figure 1A and 1B (SEQ ID NO:1).

Please amend the paragraph on lines 12-16 of page 10 to read as follows:

B₇ The "14926 receptor polypeptide" or "14926 receptor protein" refers to the polypeptide in SEQ ID NO:1. The term "receptor protein" or "receptor polypeptide", however, further includes the numerous variants described herein, as well as fragments derived from the full length 14926 polypeptide and variants.